



1	ccccccccc	GTTTGGGCCG	GGWAGCGATG	TAGTAGCTGC	CAGGCTGTCC
	CCCGCCCTGC	CCGCCCGAG	CCCCGCGGGC	CGCCGCCGCC	ACCGCCGCCA
51	TGAAGAAGCA		ATGAAGCAGC	TGGCTAACCA	GACCGTGGGC
101	AGAGCTGAGA		CCTTACTCAA	GATCTATTAC	AGATTGAGAG
151			CAATATGCCA		AAGCGCTTGG
201				ATGCCGAGAG	
251	TGGCATGTTT			ATGCAAGAAG	CATCCACTCA
301	AAACTGCCTC	TGACAGCTCT	TGCTCAAAAT		GGAGATGCTG
351	GCTGGAAGAC	TCTCTCCTGG	GGAAGATGCT		
401	AGAATCAGCT			ACGAAGTCTT	TGTTGAGAAG
451			CGGCATAGCT		TTCCCAACAT
501		AGGAAGCAGC	TTGCAAGATT		TGGGATTCAG
551	TCAGAGCCAG	GTGGAACCAA	GCTCACAAAT	CCTCAGGAAC	CAACTTTCAG
601	GGGCTTCCAT			GAAGAGATGG	ATGAAGCTGG
651		GAACAGTGCA	AGGATCAACT	TGCAGCAGAC	
701	TTATGGCCAA	AGAAGGGGAG		TCTTTGTTAC	
751	GCCCAAGCAG	ATTACCATAG	AAAAGCATTA	GCAGTCTTAG	AAAAGACCCT
801	CCCCGAAATG	CGAGCCCATC	AAGATAAGTG	GGCGGAAAAA	
851	GGACTCCCCT	AGCAGAACAC	CTGAAGAGGA	GCGGGCGCGA	
901		CCTGTGTCAT	GCTGCTTCTG	GAGACAGGCA	TGAAGGAGGA
951	GGGCCTTTTC	CGAATTGGGG	CTGGGGCCTC	CAAGTTAAAG	AAGCTGAAAG
1001	CTGCTTTGGA		TCTCACCTGG	ATGAGTTCTA	TTCAGACCCC
1051	CATGCTGTAG		AAAATCCTAT	TTACGGGAAT	TGCCTGAACC
1101	TTTGATGACT	TTTAATCTGT	ATGAAGAATG	GACACAAGTT	GCAAGTGTGC
		CAAAAAACTT	CAAGACTTGT	GGAGAACATG	
	CCACCACAAA			TTGATCAAGT	
1201	GCTTGCTCAG	ACCAGCGATG	TGAATAAAAT		AACATTGCGA
1251		CCCTAACTTG		GAAATGAAGG	
	TTGTGTTAGG		CGTCCATGTG		TTGAACCCAT
	GAAATGGCAG			AGAGGTGGAA	TTTAATGTAT
	CATTCAGCAT	GCCGACTGGT		GTTCTAATCA	
1451	CAGAAGCATT	TGTACCTCTC			
1501	ACTGGAAACG	ACTCTGACTC	GGGGACCCTG	GAGAGGAAGC	CCTCCCAAAC
1551				GAAGGAAAGT	AAACAACACTO
1601	CGAAGGACCC	TGTATCTGCA	GCTGTGCCAG	CACCAGGGAG	
1651	CAGATAGCAT	CTGGCCAAAA	TCAGCCCCAG	GCAGCTGCTG	GCTCCCACCA
1701				AGGGCCCAGC	CCGCATACAC
1751		TGTTAAAAAA			ACCGGGCAAC
1801					CATCTCAGCA
1851	TCCACCCAGT		AGCCACCCAC		TCTCCTCCCA
1901	CCCAGCACAC	GGGCCAGCCT	CCAGGCCAGC		CTCCCAGCTC
1951	TCAGCACCCC				AAGCTCCCAA
2001	TCACCCACCG	CCGCAGCCCC	CTACGCAGGC		ATGCACACCA
2051	AACCCAATAG	CCAGGGCCCT	CCCAACCCCA	TGGCATTGCC	CAGTGAGCAT
2101	GGACTTGAGC	AGCCATCTCA	CACCCCTCCC	CAGACTCCAA	CGCCCCCAG
2151	TACTCCGCCC	CTAGGAAAAC	AGAACCCCAG	TCTGCCAGCT	CCTCAGACCC
2201	TGGCAGGGG	TAACCCTGAA	ACTGCACAGC	: CACATGCTGG	AACCTTACCG
2251	AGACCGAGAC	CAGTACCAAA	GCCAAGGAAC	CGGCCCAGCG	TGCCCCCACC
2301	CCCCCAACCT	CCTGGTGTCC	ACTCAGCTGG	GGACAGCAGC	CTCACCAACA
2351	CAGCACCAAC	: AGCTTCCAAG	ATAGTAACAG	ACTCCAATTC	CAGGGTTTCA
2401	GAACCGCATC	GCAGCATCTT	TCCTGAAATG	CACTCAGACT	CAGCCAGCAA
2451	AGACGTGCCT	GGCCGCATCC	TGCTGGATAT	AGACAATGAT	ACCGAGAGCA
2501	CTCCCCTCTC	: AAGAAAGCCC	TTTCCCAGCC	CTCCACCACT	TCCACCCTGG
2501	CCACTCCACC	ACCCCCACCC	GAACCTCTTT	CTTTGCAGAC	CGAACAGTGA
2001		CTCCACCACA	AAGGAGGGCC	TCACTGTGCG	GGACCTGGCC
2001	. AAAGCIIICA	CCCAACCACA	ACCTCCACCC	CACCACTAAA	GCTGAATGAC
∠ 651		TARCARCEMENT	. ACCIGGAGGC	DTGGGDAGGA	AATCATGCCA
2/01	. CTGTGTCTTC	DOLLOHADAWA C	CTITCTITAC	THECACACACA	ATTCCTGCTG
275	AAAAAA'I'CCA	A AAACAAAGAA	MCMCCCMCC	. TARARAMANAT	CCACCACCTA
2801	AAACGCGCAT	AGGAAGCTTT	TGTCCCTGCT	CHHYYCHY GIIMMIGCGG	GCAGCACCTA
2851	CAGCAACTTG	GAATGAGTAA	A GAAGCAGTGC	CHCCHACIATC	TATTTAATAA
2903	L AATGCGCTC#	A TTATGCAAGT	CGCCTACTCT	T CTGCTACCTG	GACGTTCATT
295	L CTTATGTATI	r AGGAGGGAGG	CTGCGCTCCT	TUAGACTIGO	TGCAGAATCA
300	L TTTTGTATCA	A TGTATGGTCT	GTGTCTCCC	AGTCCCCTCA	GAACCATGCC
305	L CATGGATGG1	r GACTGCTGGC	TCTGTCACC	r catcaaacte	GATGTGACCC
310	L ATGCCGCCTC	C GTTGGATTGT	CGGAATGTAC	J ACAGAAATGI	ACTGTTCTTT

3151 TTTTTTTTT TAAACAATGT AATTGCTACT TGATAAGGAC CGAACATTAT 3201 TCTAGTTTCA TGTTTAATTT GAATTAAATA TATTCTGTGG TTTATATG

FEATURES:

5'UTR: 1-99 Start Codon: 100 Stop Codon: 2509 3'UTR: 2512

Homologous proteins:

Homologods processo.		
Top 10 BLAST Hits	Score	E
CRA 147000022595308 /altid=gi 10435148 /def=dbj BAB14506.1 (AK	1500	0.0
CRA 147000022595308 /altid=gi 10433146 /def=dbj DAB1436011 land- CRA 335001098671246 /altid=gi 11560044 /def=ref NP_071580.1 na	1331	0.0
CRA 3350010986/1246 /altid=gi 11360044 /def=fef NP_055674.1 KIAA CRA 18000005158484 /altid=gi 7662242 /def=ref NP_055674.1 KIAA	645	0.0
CRA 18000005158484 /altid=gi 7662242 /def=fef Kf_008288.1 KI CRA 335001098684832 /altid=gi 11425473 /def=ref KF_008288.1 KI	645	0.0
CRA 335001098684832 /altid=gi 11425475 /def=ref KP_007992.1 hy CRA 335001098688185 /altid=gi 11431577 /def=ref KP_007992.1 hy	452	e-126
CRA 335001098688185 /altid=gi 11431377 /def=ref NP_061830.1 SH CRA 335001098646266 /altid=gi 11545733 /def=ref NP_061830.1 SH	421	e-116
CRA 335001098646266 /altid=gi 11343733 /def=ref NP_033190.1 SH3 CRA 18000004990129 /altid=gi 6677931 /def=ref NP_033190.1 SH3	390	e-107
CRA 18000004990129 /altid=g1 6677931 /def=lef N1_03313011 State CRA 89000000202138 /altid=g1 7300563 /def=gb AAF55715.1 (AE003	264	3e-69
CRA 89000000202138 /altid=g1 7300363 /del=g5 FAN 5571511 Characteristics CRA 66000019404309 /altid=g1 8922344 /def=ref NP_060524.1 homo	251	2e-65
CRA 18000005246399 /altid=gi 7512523 /def=pir T12533 hypotheti	190	4e-47
CRA 18000005246399 /altid=g1 /512525 /del-p11 12555 m/p-0555		
EST:		
gi 10993873 /dataset=dbest /taxon=96	1524	0.0
gi 11003732 /dataset=dbest /taxon=96	1495	0.0
qi 12040806 /dataset=dbest /taxon=96	1170	0.0
gi 10948137 /dataset=dbest /taxon=96	1049	0.0
qi 11303345 /dataset=dbest /taxon=96	1043	0.0
gi 7933255 /dataset=dbest /taxon=960	918	0.0
gi 10332226 /dataset=dbest /taxon=96	912	0.0
gi 11643637 /dataset=dbest /taxon=96	906	0.0
qi 10348166 /dataset=dbest /taxon=960	664	0.0
gi 10348166 /dataset=dbest /taxon=9606	609	e-171
g1 4/535/5 /dataset-ubest /taken 5000		

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10993873 Neuronal teratocarcinoma
gi|11003732 Umbilical vein endothelial cell
gi|12040806 Iris
gi|10948137 Teratocarcinoma
gi|11303345 Breast
gi|7933255 Leiomios
gi|10332226 Uterus
gi|11643637 Kidney renal carcinoma (ascites)
gi|10348166 Uterus leiomyosarcoma
gi|4753575 Human fetal heart

Expression information from PCR-based tissue screening panels: Human leukocytes

```
1 MKKQFNRMKQ LANQTVGRAE KTEVLSEDLL QIERRLDTVR SICHHSHKRL
51 VACFQGQHGT DAERRHKKLP LTALAQNMQE ASTQLEDSLL GKMLETCGDA
101 ENQLALELSQ HEVFVEKEIV DPLYGIAEVE IPNIQKQRKQ LARLVLDWDS
151 VRARWNQAHK SSGTNFQGLP SKIDTLKEEM DEAGNKVEQC KDQLAADMYN
201 FMAKEGEYGK FFVTLLEAQA DYHRKALAVL EKTLPEMRAH QDKWAEKPAF
251 GTPLAEHLKR SGREIALPIE ACVMLLLETG MKEEGLFRIG AGASKLKKLK
301 AALDCSTSHL DEFYSDPHAV AGALKSYLRE LPEPLMTFNL YEEWTQVASV
351 QDQDKKLQDL WRTCQKLPPQ NFVNFRYLIK FLAKLAQTSD VNKMTPSNIA
401 IVLGPNLLWA RNEGTLAEMA AATSVHVVAV IEPIIQHADW FFPEEVEFNV
451 SEAFVPLTTP SSNHSFHTGN DSDSGTLERK RPASMAVMEG DLVKKESPPK
501 PKDPVSAAVP APGRNNSQIA SGQNQPQAAA GSHQLSMGQP HNAAGPSPHT
551 LRRAVKKPAP APPKPGNPPP GHPGGQSSSG TSQHPPSLSP KPPTRSPSPP
601 TQHTGQPPGQ PSAPSQLSAP RRYSSSLSPI QAPNHPPPQP PTQATPLMHT
651 KPNSQGPPNP MALPSEHGLE QPSHTPPQTP TPPSTPPLGK QNPSLPAPQT
701 LAGGNPETAQ PHAGTLPRPR PVPKPRNRPS VPPPPQPPGV HSAGDSSLTN
751 TAPTASKIVT DSNSRVSEPH RSIFPEMHSD SASKDVPGRI LLDIDNDTES
801 TAL
```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION N-glycosylation site

```
Number of matches: 6

1 13-16 NQTV
2 449-452 NVSE
3 463-466 NHSF
4 470-473 NDSD
5 515-518 NNSQ
6 796-799 NDTE
```

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site

```
Number of matches: 2

1 494-497 KKES

2 621-624 RRYS
```

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

```
Number of matches: 7
1 38-40 TVR
2 46-48 SHK
3 150-152 SVR
4 175-177 TLK
5 261-263 SGR
6 550-552 TLR
7 589-591 SPK
```

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

```
Number of matches: 14
             60-63 TDAE
             83-86 TQLE
            96-99 TCGD
      3
           109-112 SQHE
      4
           171-174 SKID
           175-178 TLKE
      6
           214-217 TLLE
      7
           233-236 TLPE
      8
           261-264 SGRE
           308-311 SHLD
     10
           349-352 SVQD
           415-418 TLAE
     12
           468-471 TGND
     13
           742-745 SAGD
     14
```

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site

117-124 KEIVDPLY

[6] PDOC00008 PS00008 MYRISTYL N-myristoylation site

```
Number of matches: 10
           56-61 GQHGTD
          251-256 GTPLAE
         290-295 GAGASK
          322-327 GALKSY
           538-543 GQPHNA
      5
           574-579 GGQSSS
      6
      7
           575-580 GQSSSG
           605-610 GQPPGQ
      8
           704-709 GNPETA
      9
           739-744 GVHSAG
     10
```

[7] PDOC00161 PS00178 AA_TRNA_LIGASE_I Aminoacyl-transfer RNA synthetases class-I signature

706-716 PETAQPHAGTL

Membranespanningstructureanddomains:HelixBeginEndScoreCertainty14154350.842Putative



>CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1| (AK023281) unnamed protein product [Homo sapiens] /org=Homo sapiens /taxon=9606 /dataset=nraa /length=726 Length = 726

Score = 1500 bits (3840), Expect = 0.0Identities = 726/726 (100%), Positives = 726/726 (100%)

idenci	CTE	, = ,23,,23 (2333,)	
Query:	78	MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ	
Sbjct:		MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEREIVDFBIGIAEVBITTIQUE	
Query:	138	RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD	197
Sbjct:		RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEGGROGERED	
		MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH	
		MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWALKTATGTT MIND	
		LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP	317
		LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSISHLDEFISDI	240
		HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLFPQNFVNFRY	377
		HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRICQKLFFQNFVNFN	300
		LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWAKNEGILAEMAAATSVHVVAVIEPIIQH	437
		LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAAISVHVVAVIEFIIQN	
		ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES	497
		ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKRES	420
		PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK	
		PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSFHILKKAVKK	
		8 PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL	
Sbjct	: 48	PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL	
Query		8 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP	
		1 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQFSHTT	000
Query	: 67	8 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP	737
		1 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPRPRNRFSVFFFFQF	000
Query	·: 73	8 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND	797
Sbjct	:: 66	PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDNE 11 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDNE	720
Query	7: 79	98 TESTAL 803	
Sbjct	:: 72	TESTAL 21 TESTAL 726	

>CRA|335001098671246 /altid=gi|11560044 /def=ref|NP_071580.1|

nadrin; neuron-specific GTPase activating protein
[Rattus norvegicus] /org=Rattus norvegicus /taxon=10116
/dataset=nraa /length=780
Length = 780

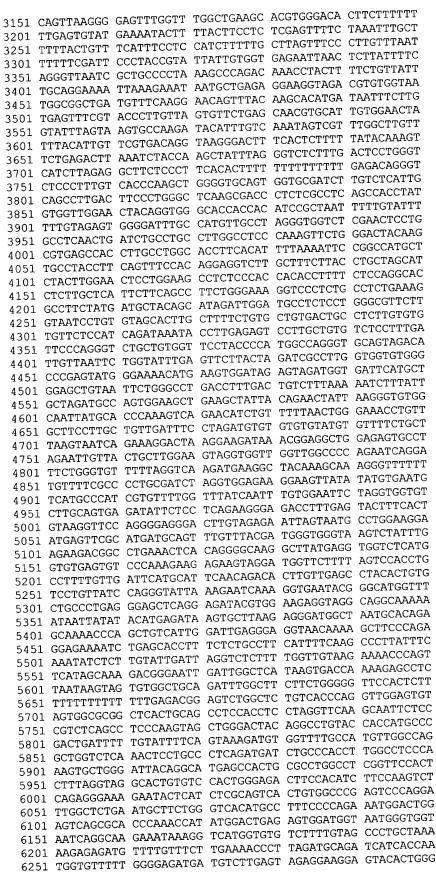
Score = 1331 bits (3406), Expect = 0.0Identities = 676/816 (82%), Positives = 697/816 (84%), Gaps = 49/816 (6%) MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSICHHSHKRLVACFQGQHGT 60 Query: 1 MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRS+CHHSHKRL+ACFQGQHGT MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSMCHHSHKRLIACFQGQHGT 60 Sbjct: 1 Query: 61 DAERRHKKLPLTALAQNMQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIV 120 DAERRHKKLPLTALAQNMQEAS QLE+SLLGKMLETCGDAENQLA ELSQHEVFVEKEI+ Sbjct: 61 DAERRHKKLPLTALAQNMQEASAQLEESLLGKMLETCGDAENQLAFELSQHEVFVEKEIM 120 Query: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM Sbjct: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180 Query: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAH 240 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEK LPEMRAH Sbjct: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKALPEMRAH 240 Query: 241 QDKWAEKPAFGTPLAEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300 QDKWAEKPAFGTPL EHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK Sbjct: 241 QDKWAEKPAFGTPLEEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300 Query: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDL 360 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTF+LYEEWTQVASVQDQDKKLQ L Sbjct: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFSLYEEWTQVASVQDQDKKLQYL 360 Query: 361 WRTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMA 420 W TCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWA+ EGTLAE+A Sbjct: 361 WTTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWAKQEGTLAEIA 420 Query: 421 AATSVHVVAVIEPIIQHADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERK 480 AATSVHVVAVIEPIIQHADWFFP EVEFNVSEAFVPL TP+SNHS HTGNDSDSGTLERK Sbjct: 421 AATSVHVVAVIEPIIQHADWFFPGEVEFNVSEAFVPLATPNSNHSSHTGNDSDSGTLERK 480 Query: 481 RPASMAVMEGDLVKKESPPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQP 540 RPASMAVMEGDLVKKESPPKPKD VSAA P GRN++QI + NQ Q Sbjct: 481 RPASMAVMEGDLVKKESPPKPKDSVSAAAPVAGRNSNQITTVPNQAQTGGNSHQLSVGTA 540 Query: 541 HNAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPP 600 H+AAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSS GT SPKP TRSPSPP Sbjct: 541 HSAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSPGT----GTSPKPSTRSPSPP 595 Query: 601 -----TQHTGQPPGQPSAPSQLSAPRRYSSSLSPIQAPNHPPPQPPTQATPL 647 Q Q Q RR SSSL PIQAPNHPPPQPPTQ Query: 648 MHTKPNSQGPPNPMALPSEHGLEQPSHTPPQTPTPPSTPPLGKQNPSLPAPQTLAGGNPE 707 +P TPPQTPTPPSTPP KQN S + OGP Sbjct: 652 --PRLGEQGP------EPGPTPPQTPTPPSTPPPAKQNSS-----QSE 686 Query: 708 TAQPHAGTLPRPRPVPKPRNRPSVPPPPQPPGVHSAGDSSLTNTAPTASKIVTDSNSRVS 767 T Q H GTLPRPRPVPKPRNRPSVPPPP PPG H GD LT + PTAS+IVTD+NSRVS Sbjct: 687 TTQLH-GTLPRPRPVPKPRNRPSVPPPPNPPGTH-MGDGGLTPSVPTASRIVTDTNSRVS 744 Query: 768 EPHRSIFPEMHSDSASKDVPGRILLDIDNDTESTAL 803 E R+IFPE+HSD ASK+VPG ILLDIDNDTESTAL Sbjct: 745 ESLRNIFPEIHSDLASKEVPGHILLDIDNDTESTAL 780

Hummer search results (Pfam):ScoreE-valueNModelDescription191.21.6e-531PF00620RhoGAP domains:

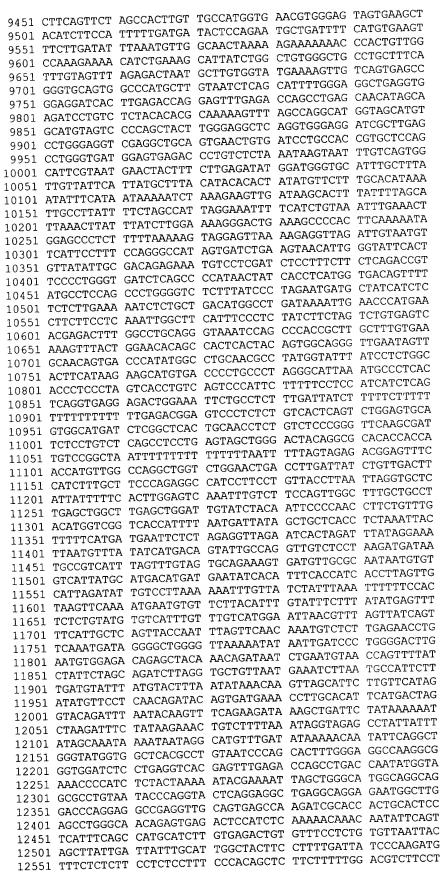
 Model
 Domain
 seq-f
 seq-t
 hmm-f
 hmm-t
 score
 E-value

 PF00620
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 266
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 170
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 191.2
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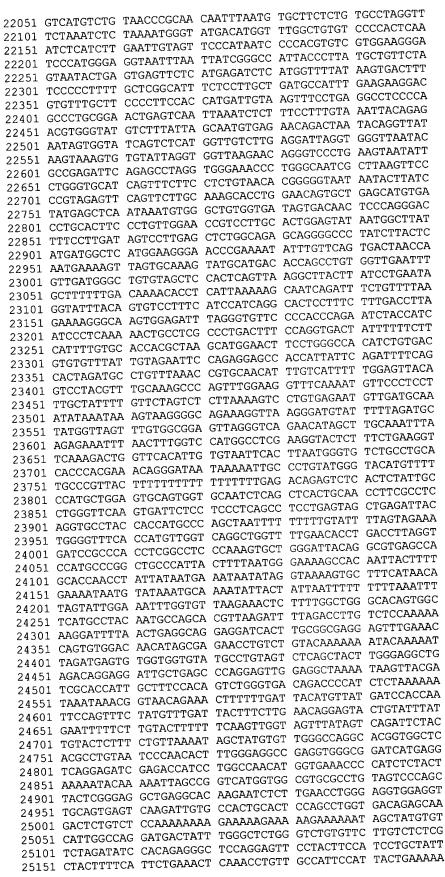


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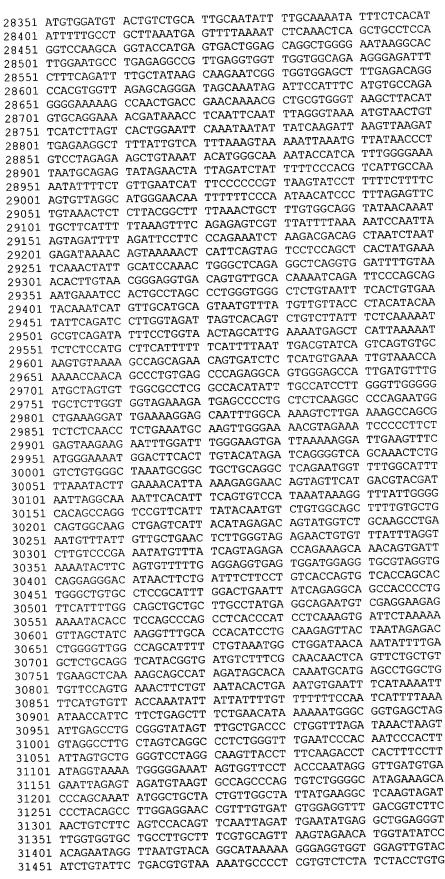


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13151	GCCTCAAACA	ACTCTCCCAT	CTTGGCCTCC	OI II II I I I I I I	GGCAGGTGAT
13201	CGTGAGCCAC	TGTGCCTGGC	CTTGAGTGAT	01111	ACACTTGAAG
13251	AGAGAATTCC	AAGGGTAGAG	ATAGTCCTAG	0001=	TTGGGAAAAA
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4 4 7 5	1 mcxmmcccc	M CTGTCGTCA	T CTGTGGAAG	I CCALCULAR	AAAAGCTTCI
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1 405	1 MCCCCAACT	ነር ጥጥጥጥሮርርCA	A AAGGTTGAG	A AAGIIGGIGG	, 10100011101
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1505	1 GGCTGAAGA	A AAGAGCAAG	G GAAGAGGTG	A GGAGCTTCA	r TTTCOUTTO
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1515	1 TTTACAAT	SA TTCCTTT'I	A GAAACATAI	A ATTGTGATA	C TTTGGGTGTG
1520)1 CTTTTATT	G GCTTTCTAT	T CTATTCCAI	T GATTTATGG	G AGTCTCGCTC
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155	51 CTGCACCT	ME CCCENCACO	TE GGTCTCTT	AC AAATACTCT	T TTTCAGGCT
450	C1 CCMMMCMC	<u>ሮሮ ሞሮ</u> እሮፎርርዊ(ST AATCCCCCA	SC ACITIGGAA	W GCIONGGGG
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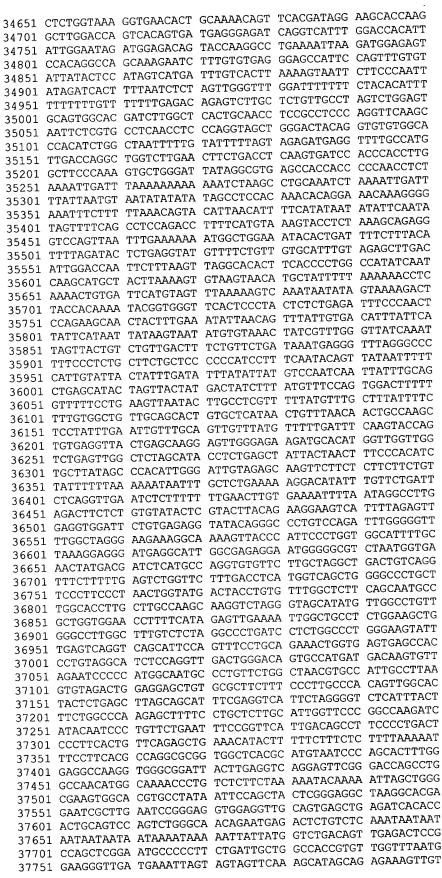
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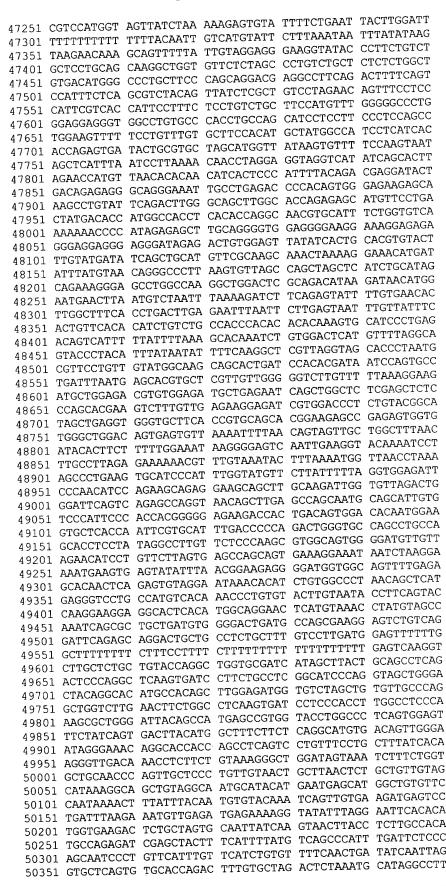
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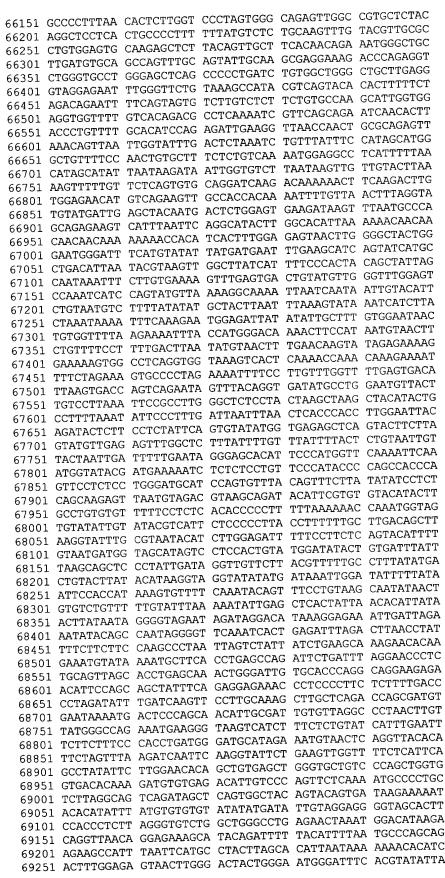
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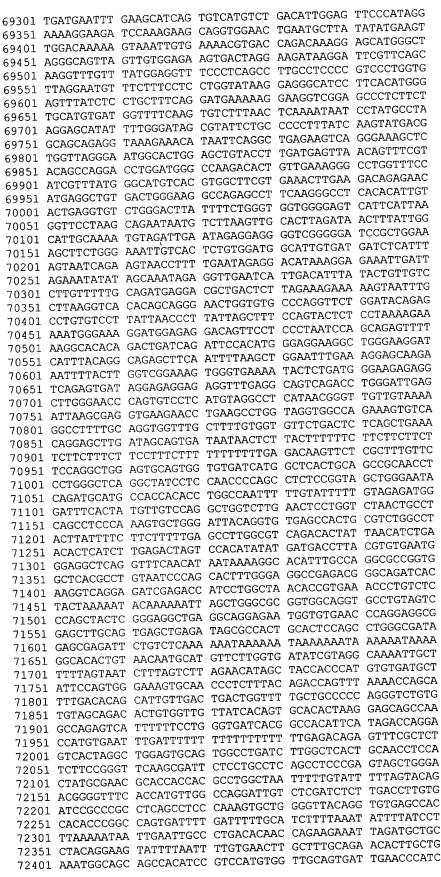


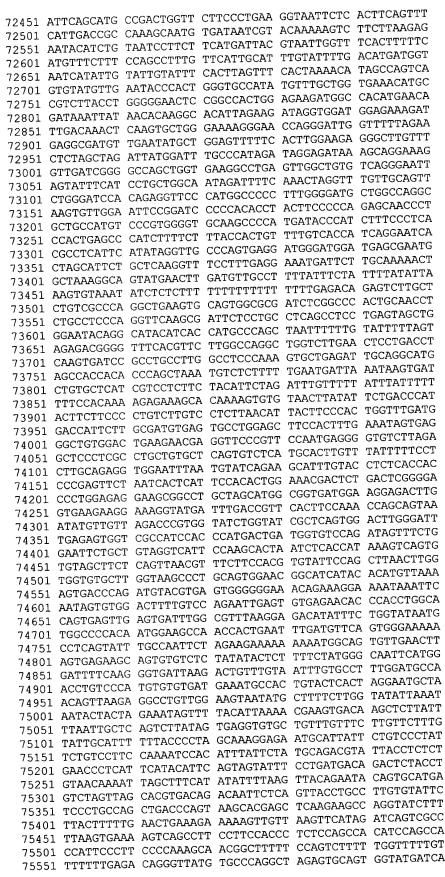
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44451 GCTGTTCACC TCTAGGAAGC ACGAAGCCCT CCCTGTGGAG GAGTTCAGTG 44501 TTGATACTTG ATTAATGAGC CCATATGTTA AGCAGAGTTT CCTTATTTAT 44551 GTACATAGGA AACAAGATTG TTGTGGCTTT GGGGTCAGGT TAGGGAAACC 44601 ACAAAACTAT TTACAGCTGC CATCTTGAGT GATGCTTGTC AAAATAGAGT 44651 TTTCTATTAT TTTTTTCCA TAGACTCCTA GAGTTCCAGA GTTGCACAAT 44701 ATATTTGTCT TGATTATTGC ATTGATCTTT AATAGGTATT TAACCTCCTT 44751 TAGAAAGGCA GCATAACCAA AAGGTAGGAA TTATCCCCTA TTATTCTCAT 44801 GTCTTCCTTG TCCAGAAATG GGGCAGCTGG GAATAGTCTC CTTGTAGTGC 44851 AGATGGAGCC CATTATTTAT TTATTTGAAA ATAATTTTGT AGGAAGCCGA 44901 GGTGGGAGGA TTGCTTGAGA CTAGGAGTTT GAGACCAGCC TGGGCAACAT 44951 AGTGAGACCT TGTCTCTACA AAAAATTTAA AAATCAATAA TTTGGGGAGA 45001 GGGGAAATGA GTAAATGCCT CTGTTTATTT TTAAATTTCA GCTTACTGTT 45051 TTGAATAGGT TCTACATTTA CACGGTCAAA ATTCAGAATA TACAAAAGAA 45101 CTTACAGTGA AGTGCCTCCT AGCCCATTTC CCCAGGCACC CAGTTCCCTC 45151 CTCCAGAGCC CCTGCTCTTA GTAGTTTGTT GTATAGCCTT GCAGAGATAT 45201 TCTGTCCAGT ACAAGCCAGT GCATATGTGA TTGTATCAGA TGGAGCCCTT 45251 TGGAGGCAGA 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46901 GATTGGTGGA AGTGGCTGGG CCAGGTGGTG TATGTAGGAC CTGTGAGAGG 46951 AACTGTGAGC GTTGATGGCA TGGCTCATCC GCTAGGAGAC CGGCTGAGAC 47001 TCCTTGGGAG AAAGTGGGGT CAAGGCCGCC AGGTTGCTGG AGAATCTTCC 47051 TTTTAGTAGG TGTCAGGCTG GAGTTGGATG GCAGAAAGGG CCATTAACAA 47101 AAAAGCAACT GATAGGGTCA ATGCCTATTC CCCTAATCTT GGACAGAAAG 47151 AATGTGGTCC CTTCTGTGTT CCAGGTGTTG GCTCAGATTT AGAAACTCTG 47201 ACCAGACCCT TTCAGTTCTT AGTCACATCG TTTACAGGCG GTCACCAAAA

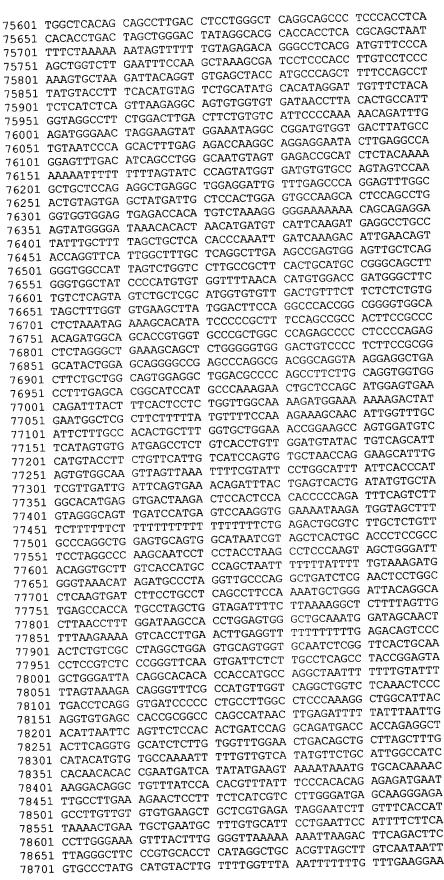


50401 TCCATGTGAC TTGGAGGGAA CAGGGTAGAG GTTAGTGTAA CATTCCCTAC 50451 TTTTGAGAGG AGACTTGTTT TACAGATAAG GGAGGGACCT GCATTTGTTA 50501 TCTATATGAC TTGCTTTGTG CCTTCAGGAG CATACATTGC AGTGTTAGGA 50551 TTCTGACAGC AAAGTCCACA GTCTCCTGGT CATGTGTACA TGTGATGTTC 50601 CCTGTCACCT GGGCTGGAGT GCAGCGGTGT GATCATAGCT CACTGCAACC 50651 TCAAACTCCT GGGCTCAAGG GATCCTCCTG CCTCAGCCTC TCGAGTAGCT 50701 GCACACCACC ACACCCAGCT ACTATTTTT TTTTTTTAA GATGGAGTCT 50751 CTCTCTGTCA ACCAGGCTGG AGTACAGTGG CACAATCTTG GCTCACTGCA 50801 ACCAAGGTGC TGGGTTCAAG CGATACTCCT GTCTCAGCCT CCTTAATAGT 50851 TGGGATTACA AGCATGTGCC ACCACACCTG GCTAATTTTT GTATTTTTAG 50901 TAGAGATGGG GTTTCACCAC ATTGGCCAGG CTGGTCTCAA ACTCCTGATC 50951 TCAGGTGATT TCCCTGCCTT AGCCTCCCAA AGTGCTAGGA TTACAGGCGT 51001 GAGCCACTGC AACCAGCCCC AGCTTTTTAT TTTTAGTAGA GACCTGGTCT 51051 CGGTATGTTG CCCAGGCTGG TCTCAAACTC CTGGCCGCAA GTAAATGTCT 51101 CTTCTTGACC TCCCACAGTG TTGGGATTAC AGGTGTGAGT CATCACACCT 51151 GGCCTGTACG TGTGATTGGA ATCCTGTGTA GCTGAGAGTG CAGGCCACCC 51201 TGCGATACAT CTTTGCTCAA GAGAAGGAAA AATATTCTAA TGATTAATTA 51251 AACAAGGCAG CAAATGCTCC CTCACTAGAG TTGGTTGAGC ATTATTATAG 51301 ATGTTTATCT GACAGGAGTT TTGCATCTTG AGTGCATGTA TCTCATAGGT 51351 GATTTTAATA CTGATTCTTG ATCTTGCATT CATGGTCTTG TTCACTTAAT 51401 CACAATAGGT GTTGGAGAAG CTGAAACAAT TGAATATTTC CACTTTTTCT 51451 CATTCTTCTT GCTTTTCCCT GGAGAAAAAA ATGGTGAATA AGTAGGAATC 51501 CATTATATGC CAGACATCAT ATGCTGTGCA CATGCACACA TATTTTTCTC 51551 GCTTTTCCTC CTTATGACAG TTCCACAAGG CAGACAGTGT TTGTGATAGT 51601 TTTGTAGATG AGGCAACTGA GATGCATAGG AGGCTAAGTC ACTAACTAGG 51651 TCACATAACT AGTTAAGATA AAGCTGAGCT CCAAACTTGA ACATGTCAGA 51701 CTCTGAAATC TATGCTCCTT TCACAATATA GCATCTCCAG TTTAGCTTTG 51751 GCTGACTTGC TGAAGCCTTT TGGTGGAGGA GTGTGTCACG TCAGGAACAC 51801 AAAGTGGGCA GAACATAGCA TTTTGGGGCA CTGCAGCAGT CTAGAAAGTT 51851 TAGTAAGTAG CTAACATGTT TTTTGGGTTT TTTTGTTTGT TTGTTTGAGA 51901 CAGGGTCTCA CTCTGTCCCC AGGCTGGAGT GCGGCGTTGC GATCTTGGTC 51951 TGGGCTCACT GCAAGCTCTG CCTCCCAGGT TCACGCCATT CTCCTGCCTC 52001 AGCCTCCCAA GTTGCTGGGA CTACAGGCGC 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52851 ATGAGAGTCC TGTCATGGTG AGAAGCTAAA GTCTCCTTTT GCCTGCTTCC 52901 ATTCTTAGAG AATAAGCTCA AGAGAATTTG GCATCCTGGG CAATGATACC 52951 CCTTCCAGGT AGAATCAATT GTGGGGAAGG ATCTATCTCC ACCAGGTCCT 53001 GCCTCCAGCT GTTGAGTATA CACAGCTGGT TCTCAGATGC TGGTGACCCC 53051 TTTGTTTTGC AGGTGGAACC AAGCTCACAA ATCCTCAGGA ACCAACTTTC 53101 AGGGGCTTCC ATCAAAAATA GATACTCTAA AGGAAGAGAT GGATGAAGCT 53151 GGAAATAAAG TAGAACAGTG CAAGGTATGA GAATTCCTTG ATAAATGTAT 53201 CTTTTCGGTT TTTGCAAATG AGGGATGAAA GTTCAAATGT AAGTTACTTA 53251 ATGTTTTAAA TAATTTCTAT CAGAATATTT TGAATGATTT TAAAGGTAGG 53301 TTTTATTTC TTCTTCTCA AGACTATATT ATTTTATGAT CAGAATAAAA 53351 CATTTTAAAT TTCAAATAGG ATATTTTTAA AAACTTGACA AGATGTCTAA 53401 GCTTATTTAA AGATGAAGTC AGAAAAAAGG AAAGAAAACC ATAGCAAAAC 53451 ATATAATAAA ATTACAGCGA TTAAAAATGC ATAAGAAATA CAAAAGTAAG 53501 AAAAAAGAAG TAAAACTGTA TAAGAAGCAT TAAAATAGAT CAGTGAAATA 53551 GTATAGGTTT TCTGGAATGA ATGCTATAAT GTAAAATTTA ATATACAGTA 53601 AATGGCTCAT ATGTCCTTGG AGAAGATAAG GATTACTTTT AAAATGTTGC 53651 TTGAACAATT 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60301 CTGAGAGTGG CTGGTGGCCT GCACCTCATT TTTGTCCCCC ACCTTCCTTT 60351 CCCTCACCCC TTTCTTCAGT CTTTACCTCT TGCTCTTTCC ATCCATTTTT 60401 ACCTTTCCAC AAGCTCTCGG TTCTATGGAT TTGTGGGATT TTATTTTTCT 60451 TCCTTCCCCA TGTGCAAATC TACCCCTGCT GTGACATGGG AGAGAGTGTA 60501 AGAGGACACA CCAGAGTACA TACTGCCTTC TTCCAACCCA GCTTTCTAAC 60551 AGCAGAGCTG CTAAGGGACC AATGGCCAGT AAAGGTGCAG AGAAGGACAT 60601 GAACCCTTCC TGTTGTTGGA AAGATTTAAG TGTTTCTCCC TGGAGCAGTT 60651 TTCACAACTG GTTTGCCCTC CTTTGCTTCT GCGAGCTGCT CAGATAGCAC 60701 TAGATCTCTG CAGCTTGCAC AGGCAGGCCA AATTCAACCA GATACTTCTT 60751 ATTCTAATTC ATATGTCCGT TCTCTAAATT CTTCTTTCTA TTTTACTGCT 60801 TCATTGTATT TGTGCTAAGC TGCCTCATAA CCTGAAGATA ATCTAAAATA 60851 TGGCTTTCCT GCCATCAGCA TAGCCTTCAG CTGCTTTAGG GCTGCAGATG 60901 CTGCATTTCT TTCCACTCAG AATTTTTCGG AGCTGTTTGG GGATGCGGTG 60951 TTCTGAAGCA CTGCATGCCG CGGAGATGTC GCATCTGATG GAGAGTAACT 61001 GCAACGTGGA GAGTTCACGT TGGCCATCTC CAGTCTTGTA TGACAGATAC 61051 TTAACTTGTG TTTGAAATTT TCAGAGATCA TTTCCATTTT TGCATAGCAA 61101 AGAATCTATT 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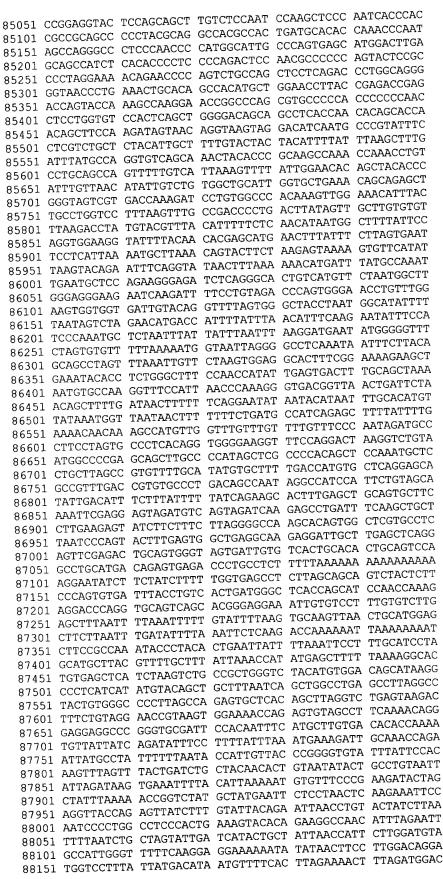






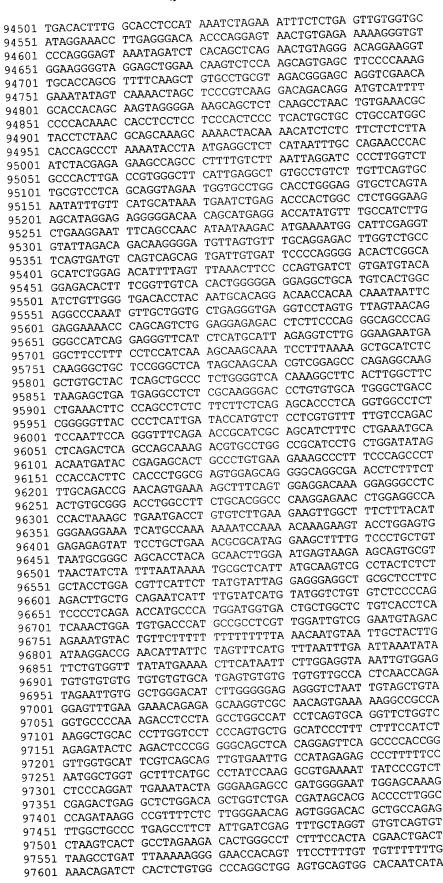


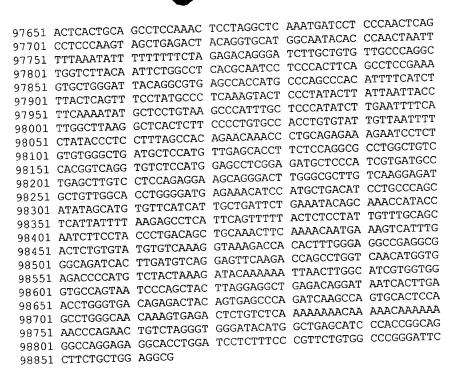
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88201	AAATTCCTGA	AAACAGGTTA	TTCCTTTAGA .	ATTGGATTAA G	TTAGAGTTT
88251	TAAAGAGTTG		AATGGGATTA	AGATAAACTC T	TGGGGGGAG
88301	ATTATTGCTG		TTGGCAGCCA	ACTTCTCACA G	CTCAGCACC
88351	AGCACTGGAG	GATGCCGGCA		11111110110	CCTGTTAAT
88401		GAGAGCAGTA	110110	1100011-	AAGAGTTTA
88451	CATCTTGCTA	TTTTTGAAGT		11001111	TTCTAATTT
88501	AAACATTTTA	TTAAATAATT		1100101	TCAGTAAGA
88551	ACTGAGATTG	GAATATTTAA	TGGTAAGGAA		TTGGCCAAT
88601	GCATTTTTGC	TACTTGATGA	TCATATTTGT	00110101111	TGTTACTAA
88651	CTGGCCACCC	TAACCCTGCC	TGCTTGCATC	• •	TGCATGCAC
88701	TGAAGGAGGA	CTGGCTTTGT	TGATGCTTGC	1001111	GGAATACTA
•	AGTGTGTACC	CAGATGTGGA		ACAGGGCTGT C	CTTGTTACT
88751	TCTTTAATTT	CCATTCTTTT	CCATATCAGG		STATAGTAGG
88801	AAGAACACAC		CAGACCTGAC		TTTCAGCTCT
88851	TGGTATAACA		ACAACCTGGC	TGATCTGTAA A	AGTGGTGACA
88901	TCTGTCTAAA			GAAAGTCCAA (SATTATTCTG
88951	TTAGCCAGTT		ATATACGCGC	AATCTCGGCT (CACTGCAAGC
89001					CTGAGTACCT
89051	TCCGCCTCCC			CTATTTTTTT '	TATTTTAGT
89101	GGGATTATAG				CTCCTGACCT
89151	AGAGACGGGG				TATAGGTGTG
89201	TAGGTGATCC				AAGAAAATAG
89251	AGCCATTGTG				TTAAAAACTC
89301					ACTGGGGGTG
89351					GTTTTTTGAA
89401					AAGGAGATAA
89451					TGAGGCGTTA
89501					GCCATAAGCC
89551					AACTCTCACC
89601					ATGAGCTGGG
89651					CTGAGGCGGG
89701					ACATGGGGAA
89751				· · · · · · · · · · · · · · · · · · ·	CGTGGTGGGT
89801		·			ACTGCTTGAA
89853					TACACTCCAG
8990					ATAAGCATGG
8995			A TGGAAATAAT		CTGTAGCTAT
9000					TTTTCTCCTC
9005					TTTTTTCAG
9010					ACGATCTTGG
9015					TGCCTCAGCC
9020	1 CTCACTGCA	A GCTCCGCCT		-	AGCTAATTTT
9025	1 TCCCGAGTA	G CTGGGACIA	C AGGCGCCCA	-	AGATGGTCTC
9030	1 TTGTATTTT	T AGTAGAGAC	A GGGTTTCAC	C GGCCTCCCAA	AGTGCTGGGA
9035	1 GATCTGCTG	A CCTTGTGAT	C ACCCGCCCC	T TTTTTTCTTT	TAGTTTTTCT
9040	1 TTACAGGCG	GAGCCACCA	C ACCATAATT	A TTTGACATAG	ACAGATTTGG
9045	1 AGAAGGCAA	G GAGGTACAI	C AUCATATIC	T CGTTCTCATG	TGATAATGTA
9050	1 ATCCTTTT	TTCACTITE	TO ATCATATOO	C ATAATGTTTC	ATCAACCAGA
9055	1 ATTTTTAGE	A CCATGITI	I CAGIGACIA	G TGGCTTCTGT	TTCTACTTGC
9060	1 TGTATTATT	A CTCCTAGTI	G GAIAIIIAA	A TTGTGTCAAG	ATAACATCCA
9065	1 AGTTTATT	TAATAAGIA	TA CTCCTCAAT	A GTTGACTCAG	AGTCTCTAAT
9070)1 GTGAGACT	rg AACAGAAT	C ANAMCAMCA	G TTCCTGATAA	AATTACACAA
9075	1 AGCCCTAGE	AA AACTGACGA	C AMENDACE	A GATTGGTTGG	ACTGTCATTC
9080)l TTCTACTT	CA ACCAAAGAC	IC MYMMMMMMCC	A GACAGAGTCT	TGCTCTGTCA
9085	1 TTCTGTTT	AT TTATTTTG	C THILLIIG	G GCACACGGCA	ACCCCTGCCT
9090)1 CCCAGGCT	AGTGCAGT	10 TOCKY1011	C CTCCCAAGTA	GCTGGGATTA
9095	ol TCCTGGTT	TA AGCAGTTC	C TIGOCIONO	T TTGTATTTT	AGTAGAGACA
9100)1 TAGGCAGG	rg regceace	CA CCCTCCTCT	C CAACTCATGA	CTTCAAGTGA
910	51 GGGTTTTG	CC ATATTGGC	CA GGCIGGICI	AG GATTACAGGO	ATGAGCCACC
911	D1 TCCACTCA	CT TUTGUUTU	CC MAAGIGCIE	T AACATTTTCO	CTCTTTCCCA
911	51 GCACCTGG	CC CCATCATT	THE COCTORCO	AT CCTGAAAGT	AAGACATTAT
912	01 AAAGAGTT	GT GTATATCC	TI GGGIGWGGY	CA CTCTGGTTA	G AGCTAAGTTT
912	51 CTGAGGAA	AT AATGGTTT	TO TABABACCI	AG AAAAAGGTTA	A TTTTAGAAAG
913	01 ATATGACA	GG TATTACAT	IG IMMAMAI DI		
					20 62

91351 ACACCTGTTA GAACCTGCTT TTTTTTTTAT TTTTTTAT TTTTGAGACT 91401 GAGTCTTACC CCGTTGCTCA GAATGGAATG CAGTGGTGCG ATCTCAGCTC 91451 ACTGTGACCT CCACCTCCCA GGTTCAAGCG ATTCTCCTGC CTCAGCCTCC 91501 TGAGTAGCTG GGATTACAGG CACTCACTAC CGTGCTCGGC TAATTTTTGT 91551 ATTTTTAGTA TAGACGGGGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC 91601 TCCTGACCTC AGGTGATCTG CCTGCCTCGG CCTCCCAAAG TGCTGGGATT 91651 ACAGGCATGA GCTACCACAC CCAGCCAGAA CCTGCTTTCT AAAAGCACCC 91701 TAAACCTCTT TGGTTGTGAA TTTATATATT CTCTGCCTTC CAAGGGCTGG 91801 AAAAAAAAA AAAACAGAAA AGAGACCTCC AATAAAAGGT TTCTTTTTTG 91851 TCTGATTTTT TGCTTTTTTT TAATTTTGAA ATATAATACT TGTCATATAA 91901 ACTTAGCTCC AAGCAGTATG CTCAAAGACC AGCCCTTCTT GGAATGCAAA 91951 TAATATATA ATTCATAGCC AGAGACGTTT AGAGGTGTTT AAAGAAAACC 92001 AGGTTCTTAC AAGTGTCTTT CTAAAATAAC CTTTATCTCT TTTTTACAAC 92051 AATCAACCAG AGTGTTTAAG ACTCAAACCG TTCACTGGTG AAGGAAGGCA 92101 TTCCCTGAGA CTCTAGGTCT GAGAAGAGGG ATGGGTGGTG GAGAGGGGGA 92151 GGGAGTTTAT TCGCCCTGCA GTTGTGCCTG CACCACTTAC TTTCAAGGGC 92201 ATATTTGGAT CTGTTACTTG TCAAAGTGGC TATCAGAATC ACCTTGGACT 92251 TCTTGAAGGG TGAGTTCACA ACCGAGAAAG CACATATTCA AAATTGTTGA 92301 AGTAATAAGT AAATCTTCTA GAACCTTACC CTCAGTGATA ACATTCCACT 92351 TCTAGCTCTT AAATACCCAC TTCTGTTTCC TGGATGAGAT ACTCAGTGCA 92401 GGAAGGAACC TGGGTTACAT TTGTCAGAGC CCCAAATCTG AGATGAACTG 92451 TATCAAGTTC TGCCTTTGGG CTGAGGCTGG TTACTGGAGG TCATCCTCTG 92501 TTTCTCTCTT TTTTTTTTT TTTTTTTTA AAAAAAAGAG AGACAGGGTC 92551 TTGCTCTGTT GCCCAGGCTA GAGTGCAGCG GTGTGATTCC AGTCCACTGC 92601 AGCCTTGACC TGCCTGGGCT CAAGCGAATC TCCCAAGTAG CTGGAAGGTG 92651 GAACTAGAGG CATGCACCAC CACACCCGGC TAATTTTTGT GTTTTTCTTA 92701 TAGAGACGGA GTCTCATGTT GCCCTGGGCT GGTCTCGAAC TTCTGGGCTC 92751 ACACCATCAT CCCACCACGC CCAGCCTATT TTGTTTTTTT AAATACAATA 92801 TCTTTTGTAT GAACTTAGCT CCAAGCATAT GCTCAGAAAC CAGCCCTTCT 92851 TGGAGTGCAG TTAATATACG AGTTCATAGC CAGAAAGATT TAGAGGTGTT 92901 TCAGACAAAC CAGGTTCTTA CAGGTGTCTT TCTGAAATAA CCATTTTCTC 92951 CTTTTTACAA CAAACCAGAG TGTTTGTAAG ACTGAAACAA TGATCTTGGA 93001 TAATGTCTTT GAAGGCCCTC ACCCAGGGAT TTACAGACTC CTCTGGGGAG 93051 GAGGGAAAAT GTAATGCGAA GAGCCAGAGT GCAACCAATC TGGCTTTGAT 93101 CCTCTTTGGT CCACACTGGC TGTGTCACCT TGGGCAAGGA ATAGAGCCTC 93151 TGAGTCTCCC TTTCTTATTT CTGCTGCCTT AGGATTAGTT AGTGGGGGTT 93201 CAGTGAGACG ATGTAATAAA GTGTGGGTGT ATAGTACAGT CTCTGGTGTA 93251 AGTAAGTGCT CTATAGTAAT GTCAGCTACT GAGGCTGGGT GTGGTGGCTC 93301 ATGCTGGTAA TCCCAGCACT TTGGGGAGCC GAGGTGGGAG GATTGCTTGA 93351 GGCCAGGAGT TCAAGACCAG CCCAGTCAAC ATGGTGAAAC CTTGTCTCTA 93401 CCAAAAATAA AAAAAATTAG CCAGGCATGG TGGCGTATGC TTGTAGTCCT 93451 AGCTACTCGG GAGGCTGAGG TGGGAGGATC AGTTGAGCCC AGGAGGTGGA 93501 GGCTGCAGTG AGCTGAGATT GCACGACTGC ACTCCAGCCT GGGCAAAAGA 93551 GCAAGACCCC ATCTCAAAAA AAAAATTTTT TTTTTTAATG TTAGCTACTG 93601 TGATGAAGTC TCTTTCTGAA AACTGGTTCT GTACAGGTTG CCGTAATTCT 93651 TTCTACTTTT TGTGTGTAAA CAAAGTCATT GTTTCTTTCA GGGACTGATT 93701 CATGTAGGAA TAGAGAGGGG CTGGGGAAAC CAGATGGGGC AGGTGGGCGG 93751 CAGAGTAAGG GATTTCCTTT ATGCCCCAAA ACACATTTTT TCCCCTTGAA 93801 TTAATAATGT GTGTGGATCA TAAATAGAAA AATTCAGAGA GGCACAAATC 93851 TAAAAATTAT GTATATGTGA TGTATAAGAA AAAGAGAGCA GCTGTGGAGG 93901 GGCTTGGTGG CTGATAGGCG TTAGCTTGCA TGTGAATACA GATATTAACA 93951 AGTAGAAATC TCATCCGTAT ACACAGTGCC TTTGCATCAT GCATTCCCCG 94001 CCAAGTCATG TCGGTTCCAT AGTTTCTGGT AAACTCTGGG CTGAGAAGAG 94051 ACACGGGCTG GTAGCCCCTT CTGTTTTTGG GGGCCAAGAT AATGGGGAAA 94101 GGATTGCATT TGCAGTGATT TTCTTATACG TCGTCTTCAA GTCACAGCTA 94151 CTTCTTTGCC TGAGGATGTA AGAATGGAGG ATTGGAAAGA TGGTTGCTCT 94201 AGATGACTCT TCATGCATCC ATCCAACCAT CCAAGTGTGC AGCTACAAAA 94251 TTTCTTGAAC ATCTGCTATT TGCCGGTCAC TGTTTTAGGT ACTGAGGATA 94351 CTTAGGACAA ATCCAAGACA GCCCCTATTC TGTGCATACA GACCACCTTT 94401 GGCTGCACCA TAGGCTGGTG CAGTTCTGCA CAGTGTCATT GGTTTTATAG 94451 TTATCACAAG ACCTGAATTG TCTGAAATGA CATTCAGCAC CTGAACTCTT





FEATURES:

2100 Start: 2100-2152 Exon: 2153-38363 Intron: 38364-38403 Exon: Intron: 38404-40049 40050-40154 Exon: 40155-46788 Intron: 46789-46862 Exon: 46863-48596 Intron: 48597-48708 Exon: 48709-48941 Intron: 48942-49018 Exon: 49019-53062 Intron: 53063-53174 Exon: 53175-56271 Intron: 56272-56340 Exon: 56341-56498 Intron: 56499-56580 Exon: Intron: 56581-61520 61521-61648 Intron: 61649-63208 63209-63320 Exon: 63321-63880 Intron: 63881-63962 Exon: 63963-66766 Intron: 66767-66847 Exon: 66848-68655 Intron: 68656-68769 Exon: 68770-72389 Intron: 72390-72481 Exon: 72482-74107 Intron: 74108-74264 Exon:





Intron: 74265-80615 Exon: 80616-80785 Intron: 80786-84851 Exon: 84852-85472 Intron: 85473-95998 Exon: 95999-96126 Stop: 96127

CHROMOSOME MAP POSITION:

Chromosome 16